

**RAW SEQUENCE LISTING  
ERROR REPORT**

BIO TECHNOLOGY  
SYSTEMS  
BRANCH

2-09-01

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/737,476

Source: OIPE

Date Processed by STIC: 01-08-01

RECEIVED

JAN 24 2001

TC 3700 MAIL ROOM

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED    SUGGESTED CORRECTION

SERIAL NUMBER: 09/737,476

| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE |                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
|------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
| 1 <input type="checkbox"/> Wrapped Nucleic                                                           | The number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".                                                                                                                                                                                                    |  |
| 2 <input type="checkbox"/> Wrapped Aminos                                                            | The amino acid number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".                                                                                                                                                                                         |  |
| 3 <input type="checkbox"/> Incorrect Line Length                                                     | The rules require that a line not exceed 72 characters in length. This includes spaces.                                                                                                                                                                                                                                                                                                                                                    |  |
| 4 <input type="checkbox"/> Misaligned Amino Acid Numbering                                           | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.                                                                                                                                                                                                                                              |  |
| 5 <input type="checkbox"/> Non-ASCII                                                                 | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.<br>Please ensure your subsequent submission is saved in ASCII text so that it can be processed.                                                                                                                                                                                                                                                            |  |
| 6 <input type="checkbox"/> Variable Length                                                           | Sequence(s) _____ contain n's or Xaa's which represented more than one residue.<br>As per the rules, each n or Xaa can only represent a single residue.<br>Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.                                                                                                                                     |  |
| 7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"                                                   | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.           |  |
| 8 <input type="checkbox"/> Skipped Sequences (OLD RULES)                                             | Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:<br>(2) INFORMATION FOR SEQ ID NO:X:<br>(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")<br>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:<br><b>This sequence is intentionally skipped</b><br><br>Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |  |
| 9 <input type="checkbox"/> Skipped Sequences (NEW RULES)                                             | Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.<br><210> sequence id number<br><400> sequence id number<br>000                                                                                                                                                                                                                                                                       |  |
| 10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)                                          | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Use of <220> to <223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.                                                                                                                                                                                           |  |
| 11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)                                         | Sequence(s) _____ are missing this mandatory field or its response.<br><br><i>Z, S, 7</i>                                                                                                                                                                                                                                                                                                                                                  |  |
| 12 <input checked="" type="checkbox"/> Use of <220>Feature (NEW RULES)                               | Sequence(s) _____ are missing the <220>Feature and associated headings.<br>Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"<br><u>Please explain source of genetic material in &lt;220&gt; to &lt;223&gt; section.</u><br>(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)                                                                                      |  |
| 13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"                                                  | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.                                                                                                                                               |  |

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/737,476

DATE: 01/08/2001  
 TIME: 17:22:26

Input Set : A:\Frenken-seq.txt  
 Output Set: N:\CRF3\01082001\I737476.raw

3 <110> APPLICANT: Unilever plc  
 4 Unilever NV  
 6 <120> TITLE OF INVENTION: Production of Antibodies  
 8 <130> FILE REFERENCE: T7060  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/737,476  
 C--> 10 <141> CURRENT FILING DATE: 2000-12-18  
 10 <160> NUMBER OF SEQ ID NOS: 67  
 12 <170> SOFTWARE: PatentIn version 3.0  
 14 <210> SEQ ID NO: 1  
 15 <211> LENGTH: 440  
 16 <212> TYPE: DNA  
 17 <213> ORGANISM: Artificial  
 19 <220> FEATURE:  
 20 <223> OTHER INFORMATION: VHH with peptide linker  
 22 <220> FEATURE:  
 23 <221> NAME/KEY: CDS  
 24 <222> LOCATION: (1)..(417)  
 26 <400> SEQUENCE: 1  
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 28 Gln Val Gin Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly  
 29 1 5 10 15  
 31 tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc aat ggt cat 96  
 32 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His  
 33 20 25 30  
 35 ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag gag cgt 144  
 36 Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg  
 37 35 40 45  
 39 gag ttt gtc gca gct att agg tgg aat ggt aaa gag aca tgg tat aaa 192  
 40 Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys  
 41 50 55 60  
 43 gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc aag act 240  
 44 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr  
 45 65 70 75 80  
 47 acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg gcc gtt 288  
 48 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val  
 49 85 90 95  
 51 tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc ctg ccg 336  
 52 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro  
 53 100 105 110  
 55 gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc tcc tca 384  
 56 Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser  
 57 115 120 125  
 59 gaa caa aaa ctc atc tca gaa gag gat ctg aat taataaggcg taagctcgaa 437  
 60 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn  
 61 130 135  
 63 ttc  
 66 <210> SEQ ID NO: 2

Does Not Comply  
 Corrected Diskette Needed

pp 2,3,4

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/737,476

DATE: 01/08/2001  
TIME: 17:22:26

Input Set : A:\Frenken-seq.txt  
Output Set: N:\CRF3\01082001\I737476.raw

67 <211> LENGTH: 139  
 68 <212> TYPE: PRT  
 69 <213> ORGANISM: Artificial  
 71 <400> SEQUENCE: 2  
 73 Gln Val Gin Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly  
 74 1 5 10 15  
 77 Ser Ile Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His  
 78 20 25 30  
 81 Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg  
 82 35 40 45  
 85 Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys  
 86 50 55 60  
 89 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr  
 90 65 70 75 80  
 93 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val  
 94 85 90 95  
 97 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro  
 98 100 105 110  
 101 Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser  
 102 115 120 125  
 105 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn  
 106 130 135  
 109 <210> SEQ ID NO: 3  
 110 <211> LENGTH: 11  
 111 <212> TYPE: PRT  
 112 <213> ORGANISM: Artificial  
 114 <220> FEATURE:  
 115 <223> OTHER INFORMATION: myc linker  
 117 <400> SEQUENCE: 3  
 119 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn  
 120 1 5 10  
 122 <210> SEQ ID NO: 4  
 123 <211> LENGTH: 471  
 124 <212> TYPE: DNA  
 125 <213> ORGANISM: Artificial  
 127 <220> FEATURE:  
 128 <223> OTHER INFORMATION: VHH with linker  
 130 <220> FEATURE:  
 131 <221> NAME/KEY: CDS  
 132 <222> LOCATION: (1)..(459)  
 134 <400> SEQUENCE: 4  
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 136 Gln Val Gin Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly  
 137 1 5 10 15  
 139 tct ctg aga ctc tcc tgt gta gct tct gaa agc agc ttc agc aac aat 96  
 140 Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn  
 141 20 25 30  
 143 cac atg ggc tgg tac cgc cgg gct cca ggg aac cag cgc gag ctg gtc 144  
 144 His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val

*MISSING mandatory <220>, <223> features  
to explain artificial sequence. See  
#12 on Error  
Summary sheet.*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/737,476

DATE: 01/08/2001  
TIME: 17:22:26

Input Set : A:\Frenken-seq.txt  
Output Set: N:\CRF3\01082001\I737476.raw

|      |       |           |            |     |     |     |     |     |     |            |     |     |     |     |     |     |     |  |
|------|-------|-----------|------------|-----|-----|-----|-----|-----|-----|------------|-----|-----|-----|-----|-----|-----|-----|--|
| 145  | 35    | 40        | 45         |     |     |     |     |     |     |            |     |     |     |     |     |     |     |  |
| 147  | gca   | act       | att        | agt | cct | ggt | ggc | aca | cac | tat        | gtt | gac | tcc | gtg | aag | 192 |     |  |
| 148  | Ala   | Thr       | Ile        | Ser | Pro | Gly | Gly | Ser | Thr | His        | Tyr | Val | Asp | Ser | Val | Lys |     |  |
| 149  | 50    |           |            |     |     |     |     |     |     |            |     |     |     |     | 60  |     |     |  |
| 151  | ggc   | cga       | tcc        | acc | atc | tcc | cga | gac | aac | gcc        | aag | aac | aca | gtg | tat | cta | 240 |  |
| 152  | Gly   | Arg       | Phe        | Thr | Ile | Ser | Arg | Asp | Asn | Ala        | Lys | Asn | Thr | Val | Tyr | Leu |     |  |
| 153  | 65    |           |            |     |     |     |     |     |     |            |     |     |     |     | 70  | 75  | 80  |  |
| 155  | caa   | atg       | gac        | agc | ctg | aaa | cca | gaa | gac | acg        | gcc | gtc | tat | tac | tgt | gct | 288 |  |
| 156  | Gln   | Met       | Asp        | Ser | Leu | Lys | Pro | Glu | Asp | Thr        | Ala | Val | Tyr | Tyr | Cys | Ala |     |  |
| 157  | 85    |           |            |     |     |     |     |     |     |            |     |     |     |     | 90  | 95  |     |  |
| 159  | gcc   | aag       | ggg        | agg | ggg | ctg | cag | gct | atg | cag        | tac | tgg | ggc | cag | ggg | acc | 336 |  |
| 160  | Ala   | Lys       | Gly        | Arg | Gly | Leu | Gln | Ala | Met | Gln        | Tyr | Trp | Gly | Glu | Gly | Thr |     |  |
| 161  | 100   |           |            |     |     |     |     |     |     |            |     |     |     |     | 105 | 110 |     |  |
| 163  | ctg   | gtc       | acc        | gtc | tcc | tca | gcy | cac | cac | agc        | gaa | gac | ccc | agc | tcc | gcg | 384 |  |
| 164  | Leu   | Val       | Thr        | Val | Ser | Ser | Ala | His | His | Ser        | Glu | Asp | Pro | Ser | Ser | Ala |     |  |
| 165  | 115   |           |            |     |     |     |     |     |     |            |     |     |     |     | 120 | 125 |     |  |
| 167  | gcc   | gcc       | cat        | cac | cat | cac | cat | cac | ggg | gcc        | gca | gaa | caa | aaa | ctc | atc | 432 |  |
| 168  | Ala   | Aia       | His        | His | His | His | His | His | Gly | Ala        | Ala | Glu | Gln | Lys | Leu | Ile |     |  |
| 169  | 130   |           |            |     |     |     |     |     |     |            |     |     |     |     | 135 | 140 |     |  |
| 171  | tca   | gaa       | qag        | gat | ctg | aat | ggg | gcc | gca | tagtaacaat | tg  |     |     |     |     |     | 471 |  |
| W--> | 172   | Ser       | Glu        | Glu | Asp | Leu | Asn | Gly | Ala | Ala        |     |     |     |     |     |     |     |  |
| 173  | 145   |           |            |     |     |     |     |     |     |            |     |     |     |     | 150 |     |     |  |
| 176  | <210> | SEQ       | ID         | NO: | 5   |     |     |     |     |            |     |     |     |     |     |     |     |  |
| 177  | <211> | LENGTH:   | 153        |     |     |     |     |     |     |            |     |     |     |     |     |     |     |  |
| 178  | <212> | TYPE:     | PRT        |     |     |     |     |     |     |            |     |     |     |     |     |     |     |  |
| 179  | <213> | ORGANISM: | Artificial |     |     |     |     |     |     |            |     |     |     |     |     |     |     |  |
| 181  | <400> | SEQUENCE: | 5          |     |     |     |     |     |     |            |     |     |     |     |     |     |     |  |
| 183  | Gln   | Val       | Gln        | Leu | Gln | Gln | Ser | Gly | Gly | Gly        | Leu | Val | Gln | Ala | Gly | Gly |     |  |
| 184  | 1     |           |            |     |     |     |     |     |     |            |     |     |     |     | 5   | 10  | 15  |  |
| 187  | Ser   | Leu       | Arg        | Leu | Ser | Cys | Val | Ala | Ser | Ser        | Phe | Ser | Asn | Asn |     |     |     |  |
| 188  |       |           |            |     |     |     |     |     |     |            |     |     |     |     | 20  | 25  | 30  |  |
| 191  | His   | Met       | Gly        | Trp | Tyr | Arg | Arg | Ala | Pro | Gly        | Asn | Gln | Arg | Glu | Leu | Val |     |  |
| 192  |       |           |            |     |     |     |     |     |     |            |     |     |     |     | 35  | 40  | 45  |  |
| 195  | Ala   | Thr       | Ile        | Ser | Pro | Gly | Gly | Ser | Thr | His        | Tyr | Val | Asp | Ser | Val | Lys |     |  |
| 196  |       |           |            |     |     |     |     |     |     |            |     |     |     |     | 50  | 55  | 60  |  |
| 199  | Gly   | Arg       | Phe        | Thr | Ile | Ser | Arg | Asp | Asn | Ala        | Lys | Asn | Thr | Val | Tyr | Leu |     |  |
| 200  |       |           |            |     |     |     |     |     |     |            |     |     |     |     | 65  | 70  | 75  |  |
| 203  | Gln   | Met       | Asp        | Ser | Leu | Lys | Pro | Glu | Asp | Thr        | Ala | Val | Tyr | Tyr | Cys | Ala |     |  |
| 204  |       |           |            |     |     |     |     |     |     |            |     |     |     |     | 85  | 90  | 95  |  |
| 207  | Ala   | Lys       | Gly        | Arg | Gly | Leu | Gln | Ala | Met | Tyr        | Trp | Gly | Gln | Gly | Thr |     |     |  |
| 208  |       |           |            |     |     |     |     |     |     |            |     |     |     |     | 100 | 105 | 110 |  |
| 211  | Leu   | Val       | Thr        | Val | Ser | Ser | Ala | His | His | Ser        | Glu | Asp | Pro | Ser | Ser | Ala |     |  |
| 212  |       |           |            |     |     |     |     |     |     |            |     |     |     |     | 115 | 120 | 125 |  |
| 215  | Ala   | Ala       | His        | His | His | His | His | Gly | Ala | Ala        | Glu | Gln | Lys | Leu | Ile |     |     |  |
| 216  |       |           |            |     |     |     |     |     |     |            |     |     |     |     | 130 | 135 | 140 |  |
| 219  | Ser   | Glu       | Glu        | Asp | Leu | Asn | Gly | Ala | Ala |            |     |     |     |     |     |     |     |  |
| 220  | 145   |           |            |     |     |     |     |     |     |            |     |     |     |     | 150 |     |     |  |
| 223  | <210> | SEQ       | ID         | NO: | 6   |     |     |     |     |            |     |     |     |     |     |     |     |  |
| 224  | <211> | LENGTH:   | 468        |     |     |     |     |     |     |            |     |     |     |     |     |     |     |  |

Missing <220>, <223>  
See #12

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/737,476

DATE: 01/08/2001  
TIME: 17:22:27

Input Set : A:\Frenken-seq.txt  
Output Set: N:\CRF3\01082001\I737476.raw

```

225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial
228 <220> FEATURE:
229 <223> OTHER INFORMATION: VHH with linker
231 <220> FEATURE:
232 <221> NAME/KEY: CDS
233 <222> LOCATION: (1)..(456)
235 <400> SEQUENCE: 6
236 cag gtg cag ctg cag gag tct ggg gga ggc ctg gtg cag gct ggg ggg      48
237 Gln Val Gln Leu Gln Glu Ser Gly Gly Leu Val Gln Ala Gly Gly
238 1           5           10          15
240 tct ctg aqa ctc tcc tgt gta gcc tct gga aac acc ttc aqt atc ata      96
241 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
242           20          25          30
244 gct atq gcc tgg tac cgc cag gct cca ggg aaq cag cgc gaa gtg gtc      144
245 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
246           35          40          45
248 gca aqt att aat aqt att ggc agc aca aat tat gca gac tcc gtg aag      192
249 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
250           50          55          60
252 ggg cga ttc acc atc tcc aga gac aac gcc aag aac aca gtc tat ctg      240
253 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
254 65           70          75          80
256 caa atg aqc agc ctg aaa cct gag gac agc gcc gtc tat tac tgt gct      288
257 Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
258           85          90          95
260 gcc ggt aat ttg ctg gtt aag agg cct tac tgg ggc cag ggg acc ctg      336
261 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
262           100         105         110
264 gtc acc gtc tcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc      384
265 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
266           115         120         125
268 gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca      432
269 Ala His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
270           130         135         140
272 gaa gag gat ctg aat ggg gca gca taataacaat tg      468
W--> 273 Glu Glu Asp Leu Asn Gly Ala Ala
274 145           150
277 <210> SEQ ID NO: 7
278 <211> LENGTH: 152
279 <212> TYPE: PRT
280 <213> ORGANISM: Artificial → See #12
282 <400> SEQUENCE: 7
284 Gln Val Gln Leu Gln Glu Ser Gly Gly Leu Val Gln Ala Gly Gly
285 1           5           10          15
288 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
289           20          25          30
292 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
293           35          40          45

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*Missing <220>, <223>*

RAW SEQUENCE LISTING DATE: 01/08/2001  
 PATENT APPLICATION: US/09/737,476 TIME: 17:22:27

Input Set : A:\Frenken-seq.txt  
 Output Set: N:\CRF3\01082001\I737476.raw

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| 296 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys |     |
| 297 50 55 60                                                        |     |
| 300 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu |     |
| 301 65 70 75 80                                                     |     |
| 304 Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala |     |
| 305 85 90 95                                                        |     |
| 308 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu |     |
| 309 100 105 110                                                     |     |
| 312 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala |     |
| 313 115 120 125                                                     |     |
| 316 Ala His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser     |     |
| 317 130 135 140                                                     |     |
| 320 Glu Glu Asp Leu Asn Gly Ala Ala                                 |     |
| 321 145 150                                                         |     |
| 324 <210> SEQ ID NO: 8                                              |     |
| 325 <211> LENGTH: 462                                               |     |
| 326 <212> TYPE: DNA                                                 |     |
| 327 <213> ORGANISM: Artificial                                      |     |
| 329 <220> FEATURE:                                                  |     |
| 330 <223> OTHER INFORMATION: VHH with linker                        |     |
| 332 <220> FEATURE:                                                  |     |
| 333 <221> NAME/KEY: CDS                                             |     |
| 334 <222> LOCATION: (1)..(450)                                      |     |
| 336 <400> SEQUENCE: 8                                               |     |
| 337 acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag | 48  |
| 338 Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln |     |
| 339 1 5 10 15                                                       |     |
| 341 gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc | 96  |
| 342 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe |     |
| 343 20 25 30                                                        |     |
| 345 agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt | 144 |
| 346 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg |     |
| 347 35 40 45                                                        |     |
| 349 gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg | 192 |
| 350 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala |     |
| 351 50 55 60                                                        |     |
| 353 gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac | 240 |
| 354 Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn |     |
| 355 65 70 75 80                                                     |     |
| 357 acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt | 288 |
| 358 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val |     |
| 359 85 90 95                                                        |     |
| 361 tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc | 336 |
| 362 Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr |     |
| 363 100 105 110                                                     |     |
| 365 gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat | 384 |
| 366 Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His |     |
| 367 115 120 125                                                     |     |
| 369 cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag | 432 |

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/737,476 DATE: 01/08/2001  
TIME: 17:22:28

Input Set : A:\Frenken-seq.txt  
Output Set: N:\CRF3\01082001\I737476.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:172 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 4  
L:273 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 6  
L:374 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 8  
L:475 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 10  
L:1684 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 66